

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Tobin, James
- (ii) TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
  - (C) REFERENCE/DOCKET NUMBER: GI5252
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 734..1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCGCCACCC CCAGCCTCTG GCAGCAGCCA GGGCATCTGG ATCTGCTTAA CTACACGCC      60
CCAGCCTGCA CCTTAGCCCC ATCCAGCTTC ACAACTGGA GACCAACGAA GTGTCAGAG      120
CCAGGCCAG CTGAGTGGCC CAACTAGCCA GACCAAGAG CCAGGTTTCAG GCGAGAAGCC      180
TGGCAGCCAG GGCAGGGGTG GGCCTCAGGG TGGGAGTGCA GGATGGGCTC AGATCCATGA      240
TGACACCCCTT CCCCACAGGCT GATAGGTTCT GCCTAGTTTA ATCAGAGCCA GTGATAAGCC      300
CTGGACCAGG TGGGGGTAAA TACCAGAAAT CCCAACAGCT GGACTGGAGG GCTTAATGGG      360
AGTGGCTGAG CTGCTGCCAG TGCTTGGTGC CAGGGGTGGG CCCCAGGGGC AGTGGAGGGG      420
GAGTTGCTGG CACAGTCTGT TCCCTCCGGC TTTTGTTCCTG GGCCTTAAGC CCAGGACTGA      480
GATGAAGGAT GTGAGGGGGT GTGTGTGTCC GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT      540
ACGCACATGC AAAGACTGG GTATACAGTG GGAAGGGGA CCTCAGGTCA GTTCCCGCAG      600

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TGAATTTCTAA CAGGCTTACC CCATCTGGTG CATCATTTTT TCTCTAGGA AGCCTCAGTT 660  
 TTGGAGAGGA AGAGCCAGGC TTTAGCCTCC CATCTCAGG GTCGGGATTT TTGACATCTA 720  
 CCTCTCCCCA CAG ATG AGC AGC AGC TCA GGG CTG AGC AGG GTC CTG 769  
 Met Ser Ser Ser Cys Ser Gly Leu Arg Val Leu 10  
 1  
 GTG GGC GTG GCT ACA GCC CTG GTG TCT GCC TCC CCC CTG CCC CCG CAG 817  
 Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Pro Cys Pro Gln 25  
 15  
 GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTC 865  
 Ala Trp Gly Pro Pro Gly Val Gly Tyr Gly Gln Pro Gly Arg Ser Val 40  
 30  
 AAG CTG TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT 913  
 Lys Leu Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe 55  
 45  
 CGG GAT GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG 961  
 Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly 75  
 65  
 CAT GAA CTG GTC CTG GCC CAG GCA AGC AGC ACT GAT GAG GGC ACC TAC 1009  
 His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr 80  
 85  
 ATC TGC CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG 1057  
 Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln 105  
 95  
 CTG GGC TAC CCT CCA GGC GGC CCT GTT GTC TCC TCC CAA CCA GCC GAC 1105  
 Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp 110  
 115  
 TAT GAG AAC TTC TCT TCC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA 1153  
 Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu 135  
 125  
 130

CCC ACC CGC TAC CTC ACC TCC TAC AGG AAG ACA GTC CTA GGA GCT  
 Pro Thr Arg Tyr 145  
 GAT AGC CAG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG  
 Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln  
 160 165 170  
 GAT CCC CTA GGG GCT GCC GGT GTC CAC GGG GGT GAG TTC TGG  
 Asp Pro Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp  
 175 180 185  
 AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GCC AGC  
 Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser  
 190 195 200  
 ACA CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA  
 Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro  
 205 210 215  
 CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CGC CTG  
 Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu  
 220 225 230 235  
 CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CGG TGC CAG CCC CAC TTC  
 Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe  
 240 245 250  
 CTG CTC AAG TTC CGT TTG CAG TAC CAT CCG GCG CAG CAT CCA GCC TGG  
 Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp  
 255 260 265  
 TCC ACG GTG GAG CCA GCT GGA CTG GAG GTG ATC ACA GAT GCT GTG  
 Ser Thr Val Glu Pro Ala Gly Leu Glu Val Ile Thr Asp Ala Val  
 270 275 280  
 GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT  
 Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp  
 285 290 295 300

1681 GCT GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC  
Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser  
315

1729 ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG  
Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr  
330

1777 CAG CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC  
Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro  
345

1825 TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG  
Ser Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu  
360

1873 CAG GTA GCT GTG GTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG  
Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu  
380

1921 GTG GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CCG GGT  
Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Gly  
395

1969 GGC AAG GAT GCA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA  
Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro  
410

2019 GTG GAC AGG GCT CCA GGA CCT CCA AAC CTG TAGAGGACCC AGGAGGCTT  
Val Asp Arg Arg Pro Gly Ala Pro Asn Leu  
420

2079 CCGCAGATTC CACCATTATAT TCTGTCITTC TGGTGTGGAT GGATGGACAG ATAGAAACCA  
GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTTG GAGCCCATTT  
CTGTGAGACC CTGTGATTTCA AATTTCACGC TCAAAAGTGC TTGTACCTCT GATTTTCACC  
CAGAGTTGGA GTTCTGCTCA AGGAAGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC

CATGTGCTG TGAGGACGG AACATGATT CTCTCATGC ATGTATGTAG GTGCTGGGG 2319  
 ACTGTGTGTC GGTCTTGGC TCTTGGCCTT TCCCTTGCA GGGTTGTGC AGGTGTGAAT 2379  
 AAGAGAAAT AGGAGTTCT TGGAGATTAT ACTCAGAAAA AAAAAAAA AGTCAGACGG 2439  
 GCGCGAATT CCTGCAG 2456

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala 15  
 1 10  
 Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro 30  
 20  
 Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys 45  
 35  
 Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu 60  
 50  
 Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val 80  
 65  
 Leu Ala Gln Ala Asp Ser Thr Asp Gln Gly Thr Tyr Ile Cys Gln Thr 95  
 85  
 Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro 110  
 100  
 105

Pro Ala Arg Pro Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe  
115 120 125

Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr  
130 135 140

Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg  
145 150 155 160

Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly  
165 170 175

Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg  
180 185 190

Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu  
195 200 205

Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Gln Gly Leu  
210 215 220

Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp  
225 230 235 240

Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe  
245 250 255

Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu  
260 265 270

Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro  
275 280 285

His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp  
290 295 300

Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile  
305 310 315 320

Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

325 330 335  
 Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro  
 340 345 350  
 His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val  
 355 360 365  
 Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala  
 370 375 380  
 Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Lys Asp Gly  
 385 390 395 400  
 Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg  
 405 410 415  
 Pro Gly Ala Pro Asn Leu  
 420

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:



TTCTTAGCCT GATAGGAGGA AGCTCTGGAG GCC ATG GCA CTC AGT CAC TGT GAT 54  
     Met Ala Leu Ser His Cys Asp 1  
     5  
 TAT CAA GAT GAG CAG CAG CTG CTC AGG GCT CAC CAG GGT CCT GGT GGC 102  
     Tyr Gln Asp Glu Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly 20  
     10  
 CGT GCT ACA GCC CTG GTG TCT TCC TCC CCC TGC CCC CAA GCT TGG 150  
     Arg Ala Thr Ala Leu Val Ser Ser Pro Cys Pro Gln Ala Trp 35  
     25  
 GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG 198  
     Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu 55  
     40  
 TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT 246  
     Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp 70  
     60  
 GGA GAT TCA AGG CTG CTC CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA 294  
     Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg 85  
     75  
 CTG GTC TTG GCC CAG CTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC 342  
     Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys 100  
     90  
 CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC 390  
     Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly 115  
     105  
 TTT CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA 438  
     Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu 135  
     120  
 AAC TTC TCC TGT ACT TGG AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC 486  
     Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr 150  
     140

CGC TAC CTT ACT TCC TAC AGG AAG AGC CTG CCA GGA GCT GAG AGT  
Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser  
155  
534

CAG AGG GAA AGT CCA TCC ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT  
Gln Arg Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro  
170  
582

CTG GAG GCC TCC CGA TGT GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG  
Leu Glu Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu  
185  
630

TAC CGG ATC AAT GTG ACC GAG GTG AAC CCA CTG GGT GCC AGC AGC TGC  
Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys  
200  
678

CTA CTG GAT GTG AGA TTA CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA  
Leu Leu Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln  
220  
726

GGA CTG CGG GTG GAA TCC GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC  
Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala  
235  
774

AGC TGG ACA TAC CCT GCC TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC  
Ser Trp Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu  
250  
822

AAG TTC CGG TTG CAA TAC CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG  
Lys Phe Arg Leu Leu Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr  
265  
870

GTG GAG CCC ATT GGC TTG GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG  
Val Glu Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly  
280  
918

CTG CCA CAC GCG GTA CGA GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC  
Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly  
300  
966

ACC TGG AGC GCC TGG AGC CCA GAG GCC TGG GGT ACT CCT ACT GGT 1014  
 Thr Trp Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly  
 315 320 325

COC CTG CAG GAG ATA CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG 1062  
 Pro Leu Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln  
 330 335 340

CTA GAG GCA GTA GTA GCT CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT 1110  
 Leu Glu Ala Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro  
 345 350 355

TCC TTG CAG CCG GAC CCA AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG 1158  
 Ser Leu Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu  
 360 365 370 375

CAA GTA GCT GTG TTA CCG TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG 1206  
 Gln Val Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu  
 380 385 390

GCT GTT GGA GCT CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CCG AGT 1254  
 Ala Val Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser  
 395 400 405

GGG AAG GAT GGA CCG CAA AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG 1302  
 Gly Lys Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro  
 410 415 420

GTG GAA AAG AGT CCA GGA ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC 1350  
 Val Glu Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn  
 425 430 435

TTT AGC TGATTTTCATC TGTAAACCCGG TCAGACTTGG GGTGGTTAAA AGGACAGGCA 1406  
 Phe Ser  
 440

GAAAGAGCG GGCAGTGGG TCCCTGTGGA TGGAGTCTC AGCTGAAAGT CTGAGCTCTT 1466  
 TTCCTTTGACA CCTATCTCC AAACCTTGGTG CCGGCTGAAG GCTGCTGGGA CTTCCGATGT 1526

CCTGAGGTGG AAGTCCACCT GAGGATGTC TACAGAAGTC TGTGTTCCCTG TGAATGCTGTG 1586  
 TGTATGTGAG ACAGGAGCA AAGTTTCTCT GCATGTGTGT ACAGATGATT GGAGACTGTG 1646  
 TGGGCTTTTG GGCATTGCCC TTCTGGGAG GTGAAGAGAGT TGAATAAAAA GAGACGGAG 1706  
 TTTTGGGA 1714

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Leu Ser His Cys Asp Tyr Gln Asp Glu Gln Leu Leu Arg 1 5 10  
 Ala Asp Gln Gly Pro Gly Arg Ala Thr Ala Leu Val Ser Ser Ser 20 25 30  
 Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln 35 40 45  
 Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser Ala Gly Thr 50 55 60  
 Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu Gln Gly Pro 65 70 75 80  
 Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val Asp Ser Pro 85 90 95  
 Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val Ser Gly Gly 100 105 110

Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro Glu Val Ser  
115 120 125

Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Gly  
130 135 140

Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys  
145 150 155 160

Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser Thr Gly Pro  
165 170 175

Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys Val Val His  
180 185 190

Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr Glu Val Asn  
195 200 205

Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu Gln Ser Ile  
210 215 220

Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly  
225 230 235 240

Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala Ser Trp Arg  
245 250 255

Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala  
260 265 270

Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu Glu Val  
275 280 285

Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg Val Ser Ala  
290 295 300

Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser Pro Glu Ala  
305 310 315 320

Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile Pro Asp Trp

325	330	335
Ser Gln Gly His Gly Gln Leu Glu Ala Val Val Ala Gln Glu Asp		
340	345	350
Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro Arg Pro Leu		
355	360	365
Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala Ser Leu Gly		
370	375	380
Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala Leu Gly Leu		
385	390	395
Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln Lys Pro Gly		
405	410	415
Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly Ile Pro Asn		
420	425	430
Leu Gln Arg Thr Pro Glu Asn Phe Ser		
435	440	